



## SEQUENCE LISTING

&lt;110&gt; Meyers, Rachel A.

&lt;120&gt; 26583, A NOVEL SERINE/THREONINE PHOSPHATASE AND USES THEREFOR

&lt;130&gt; 10448-025001

&lt;150&gt; US 60/187,454

&lt;151&gt; 2000-03-07

&lt;160&gt; 5

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 2838

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (462) ... (2072)

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (2838)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1

ggttttccac gtttgcntg accctgtttg ctcaactrwc ktytktktyk ykttytstkt	60
trygcssykw yamrakmymm rmkttkaaaa amcmrraaag ttaaytggta agtttagtct	120
ttttgtcttt tatttcaagg tcccgatcc ggtgggtggg caaatcaaag aactgctcct	180
cagtggatgt tgccttact tctaggcctg tacggaagt ttacttctgc tctaaaagct	240
gccaattct aatacactc actataggga gtcgaccac gcgtccgggt ggcaggccgg	300
gggtgagggc tcgcgtccg ggagctgcac gggctgcgt gaaaagagcg ccgagcgggt	360
gcttcgttgc cgccccctcc tcgtcgggaa gaatcgtttgc tctctctgc gtcggcggaa	420
tcccagtca g aagttccagc ctgccactgt tctctgtatgc c atg cca gca cca act	476

Met Pro Ala Pro Thr

1 5

caa ctg ttt ttt cct ctc atc cgt aac tgt gaa ctg agc agg atc tat	524
Gln Leu Phe Phe Pro Leu Ile Arg Asn Cys Glu Leu Ser Arg Ile Tyr	
10 15 20	

ggc act gca tgt tac tgc cac cac aaa cat ctc tgt tcc tca tcg	572
Gly Thr Ala Cys Tyr Cys His His Lys His Leu Cys Cys Ser Ser Ser	
25 30 35	

tac att cct cag agt cga ctg aga tac aca cct cat cca gca tat gct	620
Tyr Ile Pro Gln Ser Arg Leu Arg Tyr Thr Pro His Pro Ala Tyr Ala	
40 45 50	

acc ttt tgc agg cca aag gag aac tgg tgg cag tac acc caa gga agg	668
Thr Phe Cys Arg Pro Lys Glu Asn Trp Trp Gln Tyr Thr Gln Gly Arg	
55 60 65	

aga tat gct tcc aca cca cag aaa ttt tac ctc aca cct cca caa gtc	716
Arg Tyr Ala Ser Thr Pro Gln Lys Phe Tyr Leu Thr Pro Pro Gln Val	

70	75	80	85	
aat agc atc ctt aaa gct aat gaa tac agt ttc aaa gtg cca gaa ttt				764
Asn Ser Ile Leu Lys Ala Asn Glu Tyr Ser Phe Lys Val Pro Glu Phe				
90	95	100		
gac ggc aaa aat gtc agt tct atc ctt gga ttt gac agc aat cag ctg				812
Asp Gly Lys Asn Val Ser Ser Ile Leu Gly Phe Asp Ser Asn Gln Leu				
105	110	115		
cct gca aat gca ccc att gag gac cg <sup>g</sup> aga agt gca gca acc tgc ttg				860
Pro Ala Asn Ala Pro Ile Glu Asp Arg Arg Ser Ala Ala Thr Cys Leu				
120	125	130		
cag acc aga ggg atg ctt ttg ggg gtt ttt gat ggc cat gca ggt tgt				908
Gln Thr Arg Gly Met Leu Leu Gly Val Phe Asp Gly His Ala Gly Cys				
135	140	145		
gct tgt tcc cag gca gtc agt gaa aga ctc ttt tat tat att gct gtc				956
Ala Cys Ser Gln Ala Val Ser Glu Arg Leu Phe Tyr Tyr Ile Ala Val				
150	155	160	165	
tct ttg tta ccc cat gag act ttg cta gag att gaa aat gca gtg gag				1004
Ser Leu Leu Pro His Glu Thr Leu Leu Glu Ile Glu Asn Ala Val Glu				
170	175	180		
agc ggc cg <sup>g</sup> gca ctg cta ccc att ctc cag tgg cac aag cac ccc aat				1052
Ser Gly Arg Ala Leu Leu Pro Ile Leu Gln Trp His Lys His Pro Asn				
185	190	195		
gat tac ttt agt aag gag gca tcc aaa ttg tac ttt aac agc ttg agg				1100
Asp Tyr Phe Ser Lys Glu Ala Ser Lys Leu Tyr Phe Asn Ser Leu Arg				
200	205	210		
act tac tgg caa gag ctt ata gac ctc aac act ggt gag tcg act gat				1148
Thr Tyr Trp Gln Glu Leu Ile Asp Leu Asn Thr Gly Glu Ser Thr Asp				
215	220	225		
att gat gtt aag gag gct cta att aat gcc ttc aag agg ctt gat aat				1196
Ile Asp Val Lys Glu Ala Leu Ile Asn Ala Phe Lys Arg Leu Asp Asn				
230	235	240	245	
gac atc tcc ttg gag gcg caa gtt ggt gat cct aat tct ttt ctc aac				1244
Asp Ile Ser Leu Glu Ala Gln Val Gly Asp Pro Asn Ser Phe Leu Asn				
250	255	260		
tac ctg gtg ctt cga gtg gca ttt tct gga gcc act gct tgt gtg gcc				1292
Tyr Leu Val Leu Arg Val Ala Phe Ser Gly Ala Thr Ala Cys Val Ala				
265	270	275		
cat gtg gat ggt gtt gac ctt cat gtg gcc aat act ggc gat agc aga				1340
His Val Asp Gly Val Asp Leu His Val Ala Asn Thr Gly Asp Ser Arg				
280	285	290		
gcc atg ctg ggt gtg cag gaa gag gac ggc tca tgg tca gca gtc acg				1388
Ala Met Leu Gly Val Gln Glu Glu Asp Gly Ser Trp Ser Ala Val Thr				
295	300	305		
ctg tct aat gac cac aat gct caa aat gaa aga gaa cta gaa cgg ctg				1436
Leu Ser Asn Asp His Asn Ala Gln Asn Glu Arg Glu Leu Glu Arg Leu				
310	315	320	325	

aaa ttg gaa cat cca aag agt gag gcc aag agt gtc gtg aaa cag gat		1484	
Lys Leu Glu His Pro Lys Ser Glu Ala Lys Ser Val Val Lys Gln Asp			
330	335	340	
cg <del>g</del> ctg ctt ggc ttg ctg atg cca ttt agg gca ttt gga gat gta aag		1532	
Arg Leu Leu Gly Leu Leu Met Pro Phe Arg Ala Phe Gly Asp Val Lys			
345	350	355	
t <del>tc</del> aaa tgg agc att gac ctt caa aag aga gtg ata gaa tct ggc cca		1580	
Phe Lys Trp Ser Ile Asp Leu Gln Lys Arg Val Ile Glu Ser Gly Pro			
360	365	370	
gac cag ttg aat gac aat gaa tat acc aag ttt att cct cct aat tat		1628	
Asp Gln Leu Asn Asp Asn Glu Tyr Thr Lys Phe Ile Pro Pro Asn Tyr			
375	380	385	
cac aca cct cct tat ctc act gct gag cca gag gta act tac cac cga		1676	
His Thr Pro Pro Tyr Leu Thr Ala Glu Pro Glu Val Thr Tyr His Arg			
390	395	400	405
tta agg cca cag gat aag ttt ctg gtg ttg gct act gat ggg ttg tgg		1724	
Leu Arg Pro Gln Asp Lys Phe Leu Val Leu Ala Thr Asp Gly Leu Trp			
410	415	420	
gag act atg cat agg cag gat gtg gtt agg att gtg ggt gag tac cta		1772	
Glu Thr Met His Arg Gln Asp Val Val Arg Ile Val Gly Glu Tyr Leu			
425	430	435	
act ggc atg cat cac caa cag cca ata gct gtt ggt ggc tac aag gtg		1820	
Thr Gly Met His Gln Gln Pro Ile Ala Val Gly Gly Tyr Lys Val			
440	445	450	
act ctg gga cag atg cat ggc ctt tta aca gaa agg aga acc aaa atg		1868	
Thr Leu Gly Gln Met His Gly Leu Leu Thr Glu Arg Arg Thr Lys Met			
455	460	465	
tcc tcg gta ttt gag gat cag aac gca gca acc cat ctc att cgc cac		1916	
Ser Ser Val Phe Glu Asp Gln Asn Ala Ala Thr His Leu Ile Arg His			
470	475	480	485
gct gtg ggc aac aac gag ttt ggg act gtt gat cat gag cgc ctc tct		1964	
Ala Val Gly Asn Asn Glu Phe Gly Thr Val Asp His Glu Arg Leu Ser			
490	495	500	
aaa atg ctt agt ctt cct gaa gag ctt gct cga atg tac aga gat gac		2012	
Lys Met Leu Ser Leu Pro Glu Glu Leu Ala Arg Met Tyr Arg Asp Asp			
505	510	515	
att aca atc att gta gtt cag ttc aat tct cat gtt gta ggg gcg tat		2060	
Ile Thr Ile Ile Val Val Gln Phe Asn Ser His Val Val Gly Ala Tyr			
520	525	530	
caa aac caa gaa tagtgagtgg ctctttcact ggcaattctc aatgatata		2112	
Gln Asn Gln Glu			
535			
catttaaagg gcagat <del>ttttt</del> taaaaagata ctactataat aaacatttcc agttggc <del>tat</del>		2172	
tctaaggcatt tacccttttg atactctagc tagtcaggta ctccaaattg actttgcagc		2232	
agggtggcag ggtcaggaga gtctggctc gcctagctca gatttcatgg cacctgcact		2292	
tgaagcaagt cacttcttta tcacaggtgt cttgaaacat tagcttctt taccaacctg		2352	

agaaaattag gatgacctgg caaataagat cttgaatagg ccaaaagcaa gatatcttgct	2412
gtgtgttagtc tcttggttaa agtgaagaaa cagtagtgc cacacccccc ttcaactgaga	2472
ttccagtgtatcatgagaaca tatattttatt ksmwkrwttt yywrrtacac agtctatgca	2532
ttwttcataw wmawttattt twgcctaaat aargtkkttw wcamatcyag tthwtcmatc	2592
matraacras mamcaascaa tctrtatktr ttttktkwk trwttrwytg rmakgmwtsy	2652
twaktrrrak ramtawmcwc mstyatccay ccgmyykmvt wmykwaaktr attgaaatat	2712
tttttwtttt gccccccct tggagtcaag aagggtttt agtttatct tctyttctat	2772
tgaagttaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaaag ggcgaa	2832
	2838

<210> 2  
<211> 537  
<212> PRT  
<213> Homo sapiens

<400> 2

Met Pro Ala Pro Thr Gln Leu Phe Phe Pro Leu Ile Arg Asn Cys Glu			
1	5	10	15
Leu Ser Arg Ile Tyr Gly Thr Ala Cys Tyr Cys His His Lys His Leu			
20	25	30	
Cys Cys Ser Ser Ser Tyr Ile Pro Gln Ser Arg Leu Arg Tyr Thr Pro			
35	40	45	
His Pro Ala Tyr Ala Thr Phe Cys Arg Pro Lys Glu Asn Trp Trp Gln			
50	55	60	
Tyr Thr Gln Gly Arg Arg Tyr Ala Ser Thr Pro Gln Lys Phe Tyr Leu			
65	70	75	80
Thr Pro Pro Gln Val Asn Ser Ile Leu Lys Ala Asn Glu Tyr Ser Phe			
85	90	95	
Lys Val Pro Glu Phe Asp Gly Lys Asn Val Ser Ser Ile Leu Gly Phe			
100	105	110	
Asp Ser Asn Gln Leu Pro Ala Asn Ala Pro Ile Glu Asp Arg Arg Ser			
115	120	125	
Ala Ala Thr Cys Leu Gln Thr Arg Gly Met Leu Leu Gly Val Phe Asp			
130	135	140	
Gly His Ala Gly Cys Ala Cys Ser Gln Ala Val Ser Glu Arg Leu Phe			
145	150	155	160
Tyr Tyr Ile Ala Val Ser Leu Leu Pro His Glu Thr Leu Leu Glu Ile			
165	170	175	
Glu Asn Ala Val Glu Ser Gly Arg Ala Leu Leu Pro Ile Leu Gln Trp			
180	185	190	
His Lys His Pro Asn Asp Tyr Phe Ser Lys Glu Ala Ser Lys Leu Tyr			
195	200	205	
Phe Asn Ser Leu Arg Thr Tyr Trp Gln Glu Leu Ile Asp Leu Asn Thr			
210	215	220	
Gly Glu Ser Thr Asp Ile Asp Val Lys Glu Ala Leu Ile Asn Ala Phe			
225	230	235	240
Lys Arg Leu Asp Asn Asp Ile Ser Leu Glu Ala Gln Val Gly Asp Pro			
245	250	255	
Asn Ser Phe Leu Asn Tyr Leu Val Leu Arg Val Ala Phe Ser Gly Ala			
260	265	270	
Thr Ala Cys Val Ala His Val Asp Gly Val Asp Leu His Val Ala Asn			
275	280	285	
Thr Gly Asp Ser Arg Ala Met Leu Gly Val Gln Glu Glu Asp Gly Ser			
290	295	300	
Trp Ser Ala Val Thr Leu Ser Asn Asp His Asn Ala Gln Asn Glu Arg			
305	310	315	320
Glu Leu Glu Arg Leu Lys Leu Glu His Pro Lys Ser Glu Ala Lys Ser			
325	330	335	
Val Val Lys Gln Asp Arg Leu Leu Gly Leu Leu Met Pro Phe Arg Ala			
340	345	350	
Phe Gly Asp Val Lys Phe Lys Trp Ser Ile Asp Leu Gln Lys Arg Val			

355	360	365														
Ile	Glu	Ser	Gly	Pro	Asp	Gln	Leu	Asn	Asp	Asn	Glu	Tyr	Thr	Lys	Phe	
370							375					380				
Ile	Pro	Pro	Asn	Tyr	His	Thr	Pro	Pro	Tyr	Leu	Thr	Ala	Glu	Pro	Glu	
385								390					395			400
Val	Thr	Tyr	His	Arg	Leu	Arg	Pro	Gln	Asp	Lys	Phe	Leu	Val	Leu	Ala	
							405				410				415	
Thr	Asp	Gly	Leu	Trp	Glu	Thr	Met	His	Arg	Gln	Asp	Val	Val	Arg	Ile	
							420				425				430	
Val	Gly	Glu	Tyr	Leu	Thr	Gly	Met	His	His	Gln	Gln	Pro	Ile	Ala	Val	
							435				440				445	
Gly	Gly	Tyr	Lys	Val	Thr	Leu	Gly	Gln	Met	His	Gly	Leu	Leu	Thr	Glu	
							450				455				460	
Arg	Arg	Thr	Lys	Met	Ser	Ser	Val	Phe	Glu	Asp	Gln	Asn	Ala	Ala	Thr	
465								470				475				480
His	Leu	Ile	Arg	His	Ala	Val	Gly	Asn	Asn	Glu	Phe	Gly	Thr	Val	Asp	
							485				490				495	
His	Glu	Arg	Leu	Ser	Lys	Met	Leu	Ser	Leu	Pro	Glu	Glu	Leu	Ala	Arg	
							500				505				510	
Met	Tyr	Arg	Asp	Asp	Ile	Thr	Ile	Ile	Val	Val	Gln	Phe	Asn	Ser	His	
							515				520				525	
Val	Val	Gly	Ala	Tyr	Gln	Asn	Gln	Glu								
							530				535					

&lt;210&gt; 3

&lt;211&gt; 1611

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

atgccagcac	caactcaact	gtttttcct	ctcatccgt	actgtgaact	gaggcaggatc	60
tatggcactg	catgttactg	ccaccacaaa	catctctgtt	gttcctcatc	gtacattcct	120
cagagtcgac	tgagatacac	acctcatcca	gcatatgcta	cctttgcag	gccaaaggag	180
aactggtggc	agtacaccca	aggaaggaga	tatgcttcca	caccacagaa	atttacctc	240
acacctccac	aagtcaatag	catccttaaa	gctaataaat	acagttcaa	atgtccagaa	300
tttgacggca	aaaatgtcag	ttctatcctt	ggatttgaca	gcaatcagct	gcctgcaaata	360
gcacccattt	aggacccggag	aagtgcagca	acctgcttgc	agaccaggagg	gatgcttttg	420
ggggtttttg	atggccatgc	aggttgcgt	tgttcccagg	cagtcagtga	aagactcttt	480
tattatattt	ctgtctcttt	gttacccat	gagactttgc	tagagattga	aatgcagtg	540
gagagcggcc	gggcactgct	acccatttctc	cagtggcaca	agcacccaa	tgattacttt	600
agtaaggagg	catccaaattt	gtacttaac	agcttgagga	cttactggca	agagcttata	660
gacctaaca	ctgggtgagtc	gactgatatt	gatgttaagg	aggctcta	taatgccttc	720
aagaggcttg	ataatgacat	ctccttggag	ggcgaagttt	gtgatcctaa	ttcttttctc	780
aactacctgg	tgcttgcgt	ggcattttct	ggagccactg	cttgcgtggc	ccatgtggat	840
gttgttgacc	ttcatgtggc	caataactggc	gatagcagag	ccatgtggg	tgtgcaggaa	900
gaggacggct	catggtcagc	agtcaacgt	tctaatgacc	acaatgtca	aatgaaaga	960
gaactagaac	ggctgaaattt	ggaacatcca	aagagtgggg	ccaagagtgt	cgtgaaacag	1020
gatcggtctgc	ttggcattt	aggcatttgc	gagatgtaaa	gttcaatgg	1080	
agcattgtacc	ttcaaaaagag	agtgtatgg	tctggccctt	accagtgtaa	tgacaatgaa	1140
tataccaatgt	ttattcctcc	taattatcac	acacccctt	atctcactgc	tgagccagaa	1200
gtaacttacc	accgatataag	gccaggat	aagttctgg	tgtggctac	tgatgggttg	1260
tgggagacta	tgcataaggca	ggatgtgggt	aggattgtgg	tgagtgatct	aactggcatg	1320
catcaccaac	agccaaatagc	tgttgggtc	tacaagggtg	ctctggaca	gatgcattggc	1380
cttttaacag	aaaggagaac	caaaatgtcc	tcgttatttgc	aggatcagaa	cgcagcaacc	1440
catctcattt	gccacgcgt	gggcaacaac	gagtttggga	ctgttgcgt	tgagcgcctc	1500
tctaaaatgc	ttagttttcc	tgaagagctt	gctcgtatgt	acagagatga	cattacaatc	1560
attgttagttc	agttcaattt	tcatgttgta	ggggcgtatc	aaaaccaaga	a	1611

&lt;210&gt; 4

&lt;211&gt; 300

&lt;212&gt; PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 4

Leu Asp Val Gly Val Ser Arg Met Gln Gly Trp Arg Lys Ser Met Glu  
 1 5 10 15  
 Asp Ala His Ile Ala Leu Lys Asn Leu Asn Ser Ser Ser Ser Gly Lys  
 20 25 30  
 Asp Ser Trp Ser Phe Phe Ala Val Phe Asp Gly His Gly Ser Gln Ala  
 35 40 45  
 Ala Lys Tyr Ala Gly Lys His Leu His Lys Thr Ile Leu Ala Glu Arg  
 50 55 60  
 Lys Ser Phe Pro Glu Gly Asp Pro Trp Glu Met Lys Leu Ser Asp Leu  
 65 70 75 80  
 Glu Asp Ala Leu Lys Glu Ser Phe Leu Glu Ala Asp Thr Asp Glu Glu  
 85 90 95  
 Leu Arg Ser Ala Glu Ala Ser Ala Ala Asn Lys Val Leu Thr Lys Glu  
 100 105 110  
 Asp Leu Ser Ser Gly Ser Thr Ala Val Val Ala Leu Ile Arg Gly Asn  
 115 120 125  
 Lys Leu Tyr Val Ala Asn Val Gly Asp Ser Arg Ala Val Leu Cys Arg  
 130 135 140  
 Asn Gly Asn Ala Ile Lys Trp Ala Val Thr Leu Thr Glu Asp His Lys  
 145 150 155 160  
 Pro Ser Asn Glu Asp Glu Arg Glu Arg Ile Glu Ala Ala Gly Gly Phe  
 165 170 175  
 Val Ser Arg Val Ser Asn Gly Arg Val Asn Gly Val Leu Ala Val Ser  
 180 185 190  
 Arg Ala Phe Gly Asp Phe Glu Leu Lys Pro Gly Ser Lys Leu Gly Pro  
 195 200 205  
 Glu Glu Ser Leu Glu Ala Asn Tyr Glu Tyr Ile Lys Ser Pro Glu Gln  
 210 215 220  
 Leu Val Thr Ala Glu Pro Asp Val Thr Ser Ser Thr Asp Leu Thr Pro  
 225 230 235 240  
 Asp Lys Asp Glu Phe Leu Ile Leu Ala Cys Asp Gly Leu Trp Asp Val  
 245 250 255  
 Val Ser Asp Gln Glu Val Val Asp Ile Val Arg Ser Glu Leu Ser Asp  
 260 265 270  
 Gly Asn Lys Ser Ala Glu Asp Pro Met Glu Ala Ala Glu Lys Leu Val  
 275 280 285  
 Asp Glu Ala Ile Ala Arg Gly Ser Glu Asp Asn Ile  
 290 295 300

<210> 5

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 5

Glu Ser Ser Gly Lys Asn Leu Gly Leu Arg Tyr Gly Leu Gly Glu Ser  
 1 5 10 15  
 Ser Met Gln Gly Trp Arg Lys Pro Met Glu Asp Ala His Val Ile Arg  
 20 25 30  
 Pro Phe Phe Gly Val Phe Asp Gly His Gly Ser Glu Ala Ala Lys  
 35 40 45  
 Phe Leu Ser Lys Asn Leu His Glu Ile Leu Ala Glu Glu Leu Ser Phe

50	55	60	
Asp Lys Asp Glu Ser Leu Lys Glu Asn Glu Glu Leu Lys Asp Glu Pro			
65	70	75	80
Glu Ser Ser Glu Arg Leu Asn Gly Asp Lys Ser Leu Glu Asp Val Glu			
85	90	95	
Glu Ala Leu Arg Lys Ala Phe Leu Arg Thr Asp Glu Glu Ile Ser Thr			
100	105	110	
Ala Val Val Ala Leu Ile Arg Gly Asn Lys Leu Tyr Val Ala Asn Val			
115	120	125	
Gly Asp Ser Arg Ala Val Leu Cys Arg Asn Gly Lys Asp Ser Trp Glu			
130	135	140	
Gly Val Arg Thr Tyr Ser Ala Val Gln Leu Thr Glu Asp His Lys Pro			
145	150	155	160
Ser Asn Glu Asp Glu Arg Glu Arg Ile Glu Ala Ala Gly Gly Glu Val			
165	170	175	
Glu Pro Ile Asp Arg Glu Phe Val Ser Asn Gly Gly Val Val Trp			
180	185	190	
Arg Val Asn Gly Val Val Ile Ser Leu Ala Val Ser Arg Ala Leu Gly			
195	200	205	
Asp Phe Glu Leu Lys Lys Glu Asp Glu Leu Ile Glu Glu Asn Arg			
210	215	220	
Leu Tyr Glu Lys Phe Asp Pro Arg Leu Pro Gly Lys Glu Pro Tyr Val			
225	230	235	240
Ser Ala Glu Pro Glu Val Thr Val Val Glu Leu Ser Gln Thr Leu Val			
245	250	255	
Pro Thr Glu Asp Asp Asp Phe Leu Ile Leu Ala Ser Asp Gly Leu Trp			
260	265	270	
Asp Val Leu Ser Asn Gln Glu Ala Val Asp Ile Val Arg Lys His Leu			
275	280	285	
Arg Lys Gly Asp Asp Lys Glu Val Lys Ser Ala Ala Gln Glu Leu Ala			
290	295	300	
Arg Ala Asp Ser Leu Arg Ser Lys Lys His Asn Asp Pro Lys Glu Ala			
305	310	315	320
Ala Lys Leu Leu Val Asp Leu Ala Leu Lys Asp Asn Ile Thr Val Val			
325	330	335	
Val Val			